



RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/612,894A
Source: 1600
Date Processed by STIC: 7/3/2003

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/efc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 04/24/2003

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/612,894A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 _____ Wrapped Nucleics
 Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 _____ Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 _____ Misaligned Amino
 Numbering
The numbering under each 3rd amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 _____ Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 _____ Variable Length
Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 _____ PatentIn 2.0
 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 _____ Skipped Sequences
 (OLD RULES)
Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 _____ Skipped Sequences
 (NEW RULES)
Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 _____ Use of n's or Xaa's
 (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 _____ Invalid <213>
 Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 _____ Use of <220>
Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 _____ PatentIn 2.0
 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 _____ Misuse of n
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



1600

RAW SEQUENCE LISTING

DATE: 07/03/2003

PATENT APPLICATION: US/09/612,894A

TIME: 15:30:49

Input Set : D:\Steroidogenesis.ST25.txt

Output Set: N:\CRF4\07032003\I612894A.raw

3 <110> APPLICANT: Stocco, Douglas M
 4 <110> Clark, Barbara J
 6 <120> TITLE OF INVENTION: Compositions and Methods for Regulation of Steroidogenesis
 8 <130> FILE REFERENCE: 12491.49
 10 <140> CURRENT APPLICATION NUMBER: US 09/612,894A
 11 <141> CURRENT FILING DATE: 2000-07-10
 13 <160> NUMBER OF SEQ ID NOS: 19
 15 <170> SOFTWARE: PatentIn version 3.2
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 1466
 19 <212> TYPE: DNA
 20 <213> ORGANISM: Other nucleic acid
 22 <400> SEQUENCE: 1

invalid response - see item 10 on error summary sheet

pp 1-5
 DCCS
 Nucleic

13	tttctacccac	ggttcggtc	aggacctga	aaggctcagg	aagaacaacc	cttgagcacc	60
14	tccacactca	ggtgttctt	ggtacgttc	aagctgtgtg	ctggaagctc	ctatagacat	120
15	atggcgaata	tgaagcatt	aaggcaccac	gctgtgctgg	ccattggcca	agagctcaac	180
16	tggacagcac	tggggattc	cagtcccggt	tggatgggtc	aagttogaag	toggagctct	240
17	ctgcttggtt	ctcaactgga	agcaacactc	tatagtgaac	aggagctgtc	ctacatccag	300
18	cagggagagg	tggctatgca	gaaggccttg	ggcatactca	acaaaccagga	aggctggaag	360
19	aagaaaagcc	agcaggagaa	cggggacgaa	gtgctaagta	agatgggtgc	agatgtgggc	420
20	aagggtgttc	gcttgagggt	ggtggtagac	cagcccattg	acagactcta	tgaagaactt	480
21	gtgacccgca	tggaggccat	gggagagtgg	aaacccaaatg	tcaaggagat	caaggtccctg	540
22	cagaggattg	gaaaagacac	ggtcatcact	catgagctgg	ctgogggggc	agcaggccac	600
23	ctgctggggc	ctgagacatt	cttgagcgtg	cgtgtgaccc	agcgcagagg	ttccacctgt	660
24	tggctggcag	ggttggccac	acattctggg	gagatgcggg	agcagagtgg	tgctatccag	720
25	gcttaacagg	gccccactg	cattgtgtgt	cctccactgg	ctggaagtc	ctccaaagat	780
26	aaactcactt	ggtgtctcag	tattgacctg	aagggtgtgg	tgcgaagac	aatcatcaac	840
27	cagctccctt	cgcagaccca	gatagagttc	gcccaccacc	tgcgcaaggc	cctggaagcc	900
28	agccctgccc	ctgaggccca	gtgttaaggc	ctgtccacca	cattgacctg	caaatcattg	960
29	gaacctctca	caggaagcct	gaaagtctgt	ccatcttcag	ctaaccagcat	cgggaggggt	1020
30	ggtactcagg	agacactagg	actgactggt	aaaatcaggc	tcajcaaaat	agaaatgagg	1080
31	ctcagaatca	aggttctcta	gtgtctccca	ctgcataget	gtgaaggcta	agggataadt	1140
32	ggttctgaca	ctttctatct	aggcttgcat	atgctgacat	aaagacat	agccactacc	1200
33	aaacagggat	gctaaggatc	gggaactctt	gtcttaaccag	ctccaaatgt	cactacctga	1260
34	aaagagtggt	caacacaaag	aaggctctcc	ctaggaaact	ctgtaaaagt	tctctctgtt	1320
35	aaaggtctag	aaattcattg	aaactaccta	caaagggtct	ttccagagta	ttccaaatct	1380
36	tctctgagga	gaaatgaaac	catcatttgg	cgcacttccc	taactaatcc	atgacaataa	1440
37	aaacataaaa	taaaataaaa	aaataa				1466

74 <210> SEQ ID NO: 2
 75 <211> LENGTH: 234
 76 <212> TYPE: PRT
 77 <213> ORGANISM: amino acid
 79 <400> SEQUENCE: 1

same type of error

RAW SEQUENCE LISTING

DATE: 07/03/2003

PATENT APPLICATION: US/09/612,894A

TIME: 15:30:49

Input Set : D:\Steroidogenesis.ST25.txt

Output Set: N:\CRF4\07032003\I612894A.raw

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81 Met Phe Leu Ala Thr Phe Lys Leu Cys Ala Gly Ser Ser Tyr Arg His
82 1 5 10 15
85 Met Arg Asn Met Lys Gly Leu Arg His Gln Ala Val Leu Ala Ile Gly
86 20 25 30
89 Gln Glu Leu Asn Trp Arg Ala Leu Gly Asp Ser Ser Pro Gly Trp Met
90 35 40 45
93 Gly Gln Val Arg Arg Arg Ser Ser Leu Leu Gly Ser Gln Leu Glu Ala
94 50 55 60
97 Thr Leu Tyr Ser Asp Gln Glu Leu Ser Tyr Ile Gln Gln Gly Glu Val
98 65 70 75 80
101 Ala Met Gln Lys Ala Leu Gly Ile Leu Asn Asn Gln Glu Gly Trp Lys
102 85 90 95
105 Lys Glu Ser Gln Gln Glu Asn Gly Asp Glu Val Leu Ser Lys Met Val
106 100 105 110
109 Pro Asp Val Gly Lys Val Phe Arg Leu Glu Val Val Val Asp Gln Pro
110 115 120 125
113 Met Asp Arg Leu Tyr Glu Glu Leu Val Asp Arg Met Glu Ala Met Gly
114 130 135 140
117 Glu Trp Asn Pro Asn Val Lys Glu Ile Lys Val Leu Gln Arg Ile Gly
118 145 150 155 160
121 Lys Asp Thr Val Ile Thr His Glu Leu Ala Ala Ala Ala Gly Asn
122 165 170 175
125 Leu Val Gly Pro Arg Asp Phe Val Ser Val Arg Cys Thr Lys Arg Arg
126 180 185 190
129 Gly Ser Thr Cys Val Leu Ala Gly Met Ala Thr His Phe Gly Glu Met
130 195 200 205
133 Pro Glu Gln Ser Gly Val Ile Arg Ala Glu His Gly Pro Thr Cys Met
134 210 215 220
137 Val Leu His Pro Leu Ala Gly Ser Pro Ser Lys Thr Lys Leu Thr Trp
138 225 230 235 240
141 Leu Leu Ser Ile Asp Leu Lys Gly Trp Leu Pro Lys Thr Ile Ile Asn
142 245 250 255
145 Gln Val Leu Ser Gln Thr Gln Ile Glu Phe Ala Asn His Leu Arg Lys
146 260 265 270
149 Arg Leu Glu Ala Ser Pro Ala Ser Glu Ala Gln Cys
150 275 280
153 <10> SEQ ID NO: 3
154 <11> LENGTH: 14
155 <12> TYPE: PPT
156 <13> ORGANISM: Amino acid
157 <1400> SEQUENCE: 3
158 Ala Glu His Gly Pro Thr Cys Met Val Leu His Pro Leu Ala
159 1 10
163 <10> SEQ ID NO: 4
164 <11> LENGTH: 12
165 <12> TYPE: PPT
166 <13> ORGANISM: Amino acid
167 <1400> SEQUENCE: 4
171 Ala Leu Gly Ile Leu Asn Asn Gln Glu Gly Trp Lys

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RAW SEQUENCE LISTING

DATE: 07/03/2003

PATENT APPLICATION: US/09/612,894A

TIME: 15:30:49

Input Set : D:\Steroidogenesis.ST25.txt

Output Set: N:\CRF4\07032003\I612894A.raw

```

173 1          5          10
175 <210> SEQ ID NO: 5
176 <211> LENGTH: 19
177 <212> TYPE: PRT
178 <213> ORGANISM: Amino acid
180 <400> SEQUENCE: 5
18 Gly Ser Thr Cys Val Leu Ala Gly Met Ala Thr His Phe Gly Glu Met
181 1          5          10          15
182 <212> TYPE: PRT
183 <213> ORGANISM: Amino acid
184 <400> SEQUENCE: 6
185 Asn Gln Glu Gly Trp Lys
186 1          5
187 <210> SEQ ID NO: 6
188 <211> LENGTH: 9
189 <212> TYPE: PRT
190 <213> ORGANISM: Amino acid
191 <400> SEQUENCE: 7
192 Ala Glu His Gly Pro Thr Cys Met Val
193 1          5
194 <210> SEQ ID NO: 8
195 <211> LENGTH: 11
196 <212> TYPE: PRT
197 <213> ORGANISM: Amino acid
198 <400> SEQUENCE: 8
199 Ile Leu Asn Asn Gln Glu Gly Trp Lys Lys Glu
200 1          5          10
201 <210> SEQ ID NO: 9
202 <211> LENGTH: 15
203 <212> TYPE: DNA
204 <213> ORGANISM: other nucleic acid
205 <214> FEATURE:
206 <215> NAME/KEY: misc_feature
207 <216> LOCATION: (3)..(3)
208 <233> OTHER INFORMATION: n = (a or c or g or t/u) or (unknown or other)
209 <220> FEATURE:
210 <221> NAME/KEY: modified_base
211 <222> LOCATION: (6)..(6)
212 <233> OTHER INFORMATION: r = a or c
213 <220> FEATURE:
214 <221> NAME/KEY: modified_base
215 <222> LOCATION: (9)..(9)
216 <233> OTHER INFORMATION: y = c or t/u
217 <220> FEATURE:
218 <221> NAME/KEY: misc_feature
219 <222> LOCATION: (12)..(12)

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RAW SEQUENCE LISTING

DATE: 07/03/2003

PATENT APPLICATION: US/09/612,894A

TIME: 15:30:49

Input Set : D:\Steroidogenesis.ST25.txt

Output Set: N:\CRF4\07032003\I612894A.raw

147 <223> OTHER INFORMATION: n = (a or c or g or t/u) or (unknown or other)
 149 <220> FEATURE:
 150 <221> NAME/KEY: misc_feature
 151 <222> LOCATION: (15)..(15)
 152 <223> OTHER INFORMATION: n = (a or c or g or t/u) or (unknown or other)
 154 <220> FEATURE:
 155 <221> NAME/KEY: misc_feature
 156 <222> LOCATION: (16)..(16)
 157 <223> OTHER INFORMATION: n = (a or c or g or t/u) or (unknown or other)
 159 <220> FEATURE:
 160 <221> NAME/KEY: modified_base
 161 <222> LOCATION: (21)..(21)
 162 <223> OTHER INFORMATION: y = c or t/u
 164 <400> SEQUENCE: 9

W--> 265 gcngarcayg gncnacntg yatgg

25

165 <10> SEQ ID NO: 19
 166 <11> LENGTH: 25
 167 <12> TYPE: DNA
 171 <13> ORGANISM: other nucleic acid
 173 <220> FEATURE:
 175 <221> NAME/KEY: modified_base
 176 <222> LOCATION: (5)..(5)
 177 <223> OTHER INFORMATION: r = a or g
 179 <220> FEATURE:
 180 <221> NAME/KEY: misc_feature
 181 <222> LOCATION: (8)..(8)
 182 <223> OTHER INFORMATION: r = (a or c or g or t/u) or (unknown or other)
 184 <220> FEATURE:
 185 <221> NAME/KEY: misc_feature
 186 <222> LOCATION: (11)..(11)
 187 <223> OTHER INFORMATION: r = (a or c or g or t/u) or (unknown or other)
 189 <220> FEATURE:
 190 <221> NAME/KEY: misc_feature
 191 <222> LOCATION: (14)..(14)
 192 <223> OTHER INFORMATION: r = (a or c or g or t/u) or (unknown or other)
 194 <220> FEATURE:
 195 <221> NAME/KEY: modified_base
 196 <222> LOCATION: (17)..(17)
 197 <223> OTHER INFORMATION: r = a or g
 199 <220> FEATURE:
 200 <221> NAME/KEY: modified_base
 201 <222> LOCATION: (19)..(20)
 202 <223> OTHER INFORMATION: y = c or t/u
 204 <220> FEATURE:
 205 <221> NAME/KEY: misc_feature
 206 <222> LOCATION: (23)..(23)
 207 <223> OTHER INFORMATION: n = (a or c or g or t/u) or (unknown or other)
 209 <400> SEQUENCE: 19

W--> 310 ccatrcangt nggncrtgy tcnge

25

RAW SEQUENCE LISTING

DATE: 07/03/2003

PATENT APPLICATION: US/09/612,894A

TIME: 15:30:49

Input Set : D:\Steroidogenesis.ST25.txt

Output Set: N:\CRF4\07032003\I612894A.raw

313 <210> SEQ ID NO: 11
 314 <211> LENGTH: 17
 315 <212> TYPE: DNA
 316 <213> ORGANISM: other nucleic acid
 319 <210> FEATURE:
 321 <211> NAME/KEY: modified_base
 321 <212> LOCATION: (15)..(15)
 322 <213> OTHER INFORMATION: y = c or t/u
 324 <210> FEATURE:
 325 <211> NAME/KEY: modified_base
 326 <212> LOCATION: (6)..(6)
 327 <213> OTHER INFORMATION: r = a or g
 329 <210> FEATURE:
 330 <211> NAME/KEY: modified_base
 331 <212> LOCATION: (9)..(9)
 332 <213> OTHER INFORMATION: r = a or g
 334 <210> FEATURE:
 335 <211> NAME/KEY: misc_feature
 336 <212> LOCATION: (12)..(12)
 337 <213> OTHER INFORMATION: n = (a or c or g or t/u) or (unknown or other)
 339 <400> SEQUENCE: 11

W--> 340 aaycarcarg gntggaa

17

341 <210> SEQ ID NO: 12
 342 <211> LENGTH: 17
 343 <212> TYPE: DNA
 344 <213> ORGANISM: other nucleic acid
 347 <210> FEATURE:
 349 <211> NAME/KEY: misc_feature
 350 <212> LOCATION: (6)..(6)
 351 <213> OTHER INFORMATION: n = (a or c or g or t/u) or (unknown or other)
 353 <210> FEATURE:
 354 <211> NAME/KEY: modified_base
 355 <212> LOCATION: (3)..(3)
 356 <213> OTHER INFORMATION: y = c or t/u
 358 <210> FEATURE:
 359 <211> NAME/KEY: modified_base
 360 <212> LOCATION: (12)..(12)
 361 <213> OTHER INFORMATION: y = c or t/u
 363 <210> FEATURE:
 364 <211> NAME/KEY: modified_base
 365 <212> LOCATION: (15)..(15)
 366 <213> OTHER INFORMATION: r = a or g
 368 <400> SEQUENCE: 12

W--> 370 ttccanccyt cytgrrt

17

371 <210> SEQ ID NO: 13
 372 <211> LENGTH: 401
 373 <212> TYPE: DNA
 374 <213> ORGANISM: other nucleic acid
 376 <400> SEQUENCE: 13

Please correct
 this type of error
 in subsequent sequences

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/612,894A

DATE: 07/03/2003
TIME: 15:30:50

Input Set : D:\Steroidogenesis.ST25.txt
Output Set: N:\CRF4\07032003\I612894A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:9; N Pos. 3,12,15,18
Seq#:10; N Pos. 8,11,14,23
Seq#:11; N Pos. 12
Seq#:12; N Pos. 6